CLAIMS

What is claimed is:

1. A carotenoid overproducing bacteria comprising the genes encoding a functional carotenoid enzymatic biosynthetic pathway wherein the *dxs, idi* and *ygbBP* genes are overexpressed and wherein the *yjeR* gene is down regulated.

2. A carotenoid overproducing bacteria comprising the genes encoding a functional carotenoid enzymatic biosynthetic pathway wherein the *dxs, idi, ygbBP* and *ispB* genes are overexpressed.

3. The carotenoid overproducing bacteria of Claim 1 or 2 wherein the *lytB* and *dxr* gene is optionally overexpressed.
ispB lytB and *dxr yjeR*

4. The carotenoid overproducing bacteria of Claim 1 or 2 wherein the carotenoid enzymatic biosynthetic pathway consists of the genes *dxs, dxr, ygpP, ychB, ygbB, lytB, idi, ispA, ispB crtE, crtB, crtI,* and *crtY.*

5. The carotenoid overproducing bacteria of Claim 4 wherein the carotenoid enzymatic biosynthetic pathway optionally additionally comprises the *crtZ* and *crtW* genes.

6. The carotenoid overproducing bacteria of any of Claims 1-5 wherein the bacteria is selected from the group consisting *Agrobacterium, Erythrobacter, Chlorobium, Chromatium, Flavobacterium, Cytophaga, Rhodobacter, Rhodococcus, Streptomyces, Brevibacterium, Corynebacteria, Mycobacterium, Deinococcus, Paracoccus, Escherichia, Bacillus, Myxococcus, Salmonella, Yersinia, Erwinia, Pantoea, Pseudomonas, Sphingomonas, Methylomonas, Methylobacter, Methylococcus, Methylosinus, Methylomicrobium, Methylocystis, Alcaligenes, Synechocystis, Synechococcus, Anabaena, Thiobacillus, Methanobacterium, Klebsiella,* and *Myxococcus.*

7. The carotenoid overproducing bacteria of Claim 6 wherein the bactera is *E. coli.*

8. The carotenoid overproducing bacteria of Claims 1-3 wherein the *dxs, dxr, ygpP, ychB, ygbB, lytB, idi, ispA, ispB* are derived from a *Methylomonas sp..*

9. The carotenoid overproducing bacteria of any of Claims 1 – 3 wherein the *dxs, idi, ispB* and *ygbBP* genes are under the control of a strong promoter.

10. The carotenoid overproducing bacteria of Claim 9 wherein the strong promoter is selected from the group consisting of *lac*, *ara*, *tet*, *trp*, λP_L, λP_R, *T7*, *tac*, P_{T5}, and *trc*.

11. The carotenoid overproducing bacteria of any of Claims 1-3 wherein the *dxs, idi, ispB* and *ygbBP* genes are integrated in multicopy in the bacterial chromosome.

12. The carotenoid overproducing bacteria of any of Claims 1-3 wherein the *dxs, idi, ispB* and *ygbBP* genes are present in multicopy in the bacteria on one or more plasmids.

13. The carotenoid overproducing bacteria of of Claim 7 wherein the *yjeR* gene is down regulated by gene disruption.

14. The carotenoid overproducing bacteria of Claim 13 wherein the disrupted *yjeR* gene has the nucleotide sequence as set forth in SEQ ID NO:63.

15. The carotenoid overproducing bacteria of either of any of Claims 1 –3 wherein the *dxs, idi, ispB ygbBP* and *lytB* genes are chromosomally integrated into the host cell genome.

16. A carotenoid overproducing bacteria selected from the group consisting of: a strain having the ATCC identification number PTA-4807 and a strain having the ATCC identification number PTA-4823.

17. A method for the production of a carotenoid comprising:

a) growing the carotenoid overproducing bacteria of any of Claims 1 –5, the bacteria overexpressing at least one gene selected from the group consisting of *dxs, idi ygbBP, ispB, lytB, dxr,* wherein *yjeR* is optionally downregulated, for a time sufficient to produce a carotenoid; and

b) optionally recovering the carotenoid from the carotenoid overproducing bacteria of step (a).

18. A method according to Claim 17 wherein the carotenoid is selected from the group consisting of antheraxanthin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin, β-cryptoxanthin, didehydrolycopene, didehydrolycopene, β-carotene, ζ–carotene, δ–carotene, γ–carotene, keto–γ–carotene, ψ–carotene, ε–carotene, β,ψ–carotene, torulene, echinenone, gamma-carotene, zeta-carotene, alpha-cryptoxanthin, diatoxanthin, 7,8-didehydroastaxanthin, fucoxanthin, fucoxanthinol, isorenieratene, β-isorenieratene lactucaxanthin, lutein, lycopene, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene,

rhodopin, rhodopin glucoside, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, uriolide, uriolide acetate, violaxanthin, zeaxanthin-β-diglucoside, zeaxanthin, and C30-carotenoids.

19. A method according to Claim 18 wherein the carotenoid is produced at a level of at least about 6 mg per gram dry cell weight.

20. A method according to Claim 18 wherein the bacteria is selected from the group consisting *Agrobacterium, Erythrobacter, Chlorobium, Chromatium, Flavobacterium, Cytophaga, Rhodobacter, Rhodococcus, Streptomyces, Brevibacterium, Corynebacteria, Mycobacterium, Deinococcus, Paracoccus, Escherichia, Bacillus, Myxococcus, Salmonella, Yersinia, Erwinia, Pantoea, Pseudomonas, Sphingomonas, Methylomonas, Methylobacter, Methylococcus, Methylosinus, Methylomicrobium, Methylocystis, Alcaligenes, Synechocystis, Synechococcus, Anabaena, Thiobacillus, Methanobacterium, Klebsiella,* and *Myxococcus.*

21. A method according to Claim 20 wherein the bacteria is *E. coli.*

22. A method according to Claim 17 wherein the *dxs, idi, ygbBP, ispB* and *lytB* genes are under the control of a promoter selected from the group consisting of *lac*, *ara*, *tet*, *trp*, λP_L, λP_R, *T7*, *tac*, P_{T5}, and *trc.*

23. A method according to Claim 17 wherein the *dxs, idi, ispB, ygbBP* and *lytB* genes are integrated in multicopy in the bacterial chromosome.

24. A method according to Claim 17 wherein the *dxs, idi, ispB, ygbBP* and *lytB* genes are in multicopy in the bacteria on one or more plasmids.

25. A method according to Claim 17 wherein the *yjeR* gene is down regulated by gene disruption.

26. A method according to Claim 25 wherein the disrupted *yjeR* gene has the nucleotide sequence as set forth in SEQ ID NO:63.

27. A method according to Claim 17 wherein the *dxs, idi ispB, ygbBP* and *lytB* genes are chromosomally integrated into the host cell genome.